seed size. Selection of accessions with large bolls might result in lower elongation, 50% span length and fiber strength. Seed size was positively correlated with micronaire for accessions or with elongation for accessions in some environments ($\hat{R}_{AE} = 0.74^{**}$). Simultaneous improvement was possible for fiber strength with 50% span length while selecting accessions or generations in accessions, and with 2.5% span length while selecting generations in accessions. Highly positive correlations were observed for R_A and R_{AG} between 50 and 2.5% span length.

Since there were large interaction between accession generation for the yield and fiber traits studied, evaluation of accessions should be considered for specific generations. We will predict breeding merits for accessions, generations, and their combinations in a companion paper (McCarty et al., 1998).

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Introgression of Day-Neutral Genes in Primitive Cotton Accessions: II. Predicted Genetic Effects

J. C. McCarty, Jr.,* J. N. Jenkins, and J. Zhu

ABSTRACT

Primitive accessions of cotton, *Gossypium hirsutum* L., may provide useful traits for cultivar development. Genetic effects for yield, yield components, and fiber traits were analyzed for five generations of day-neutral progenies. The genetic material was derived from introgressing day-neutral genes from 'Deltapine 16' into 16 primitive accessions with single and multiple backcrosses creating 80 populations representing one to four doses of the unadapted accession. Yield and fiber traits were determined from field plot studies conducted for 3 yr. Significant accession effects were detected for all the traits studied. Significant generation main effects were found for three yield traits and one fiber trait. As expected, yield was predicted to decrease with more cycles of backcrossing to the accession. Accessions × generation interactions were detected for some traits which indicated that not all generations were having equal effects. This genetic analysis provides useful information when utilizing these accessions.

A NARROW GENETIC BASE could result in crop cultivars being highly vulnerable to stresses and it could also restrict genetic gain. Therefore, it is important that we expand the genetic diversity of cotton with new and unrelated sources of germplasm. Primitive accessions of cotton are an important source of useful genetic variability (Percival, 1987; Meredith, 1991; McCarty and Jenkins, 1992; McCarty et al., 1995). Percival and Kohel (1990) reviewed the collection, distribution, and evaluation of *Gossypium* germplasm.

Most tropical primitive accessions of cotton are perennial, photoperiod sensitive, and do not flower under the long days of the U.S. cotton belt. In their native habitat they flower during short days in winter months and remain vegetative during long summer days. The use of these primitive accessions has been limited because of their flowering response. A backcross-breeding program has been in place for a number of years to incorporate day-neutral genes into the primitive accessions (McCarty et al., 1979; McCarty and Jenkins, 1992, 1993).

McCarty et al. (1995) evaluated F_5, BC_1F_5, BC_2F_5, BC_3F_5, and BC_4F_5 progenies of 16 day-neutral germplasm accessions for several agronomic and fiber traits. Results indicated there was useful variability for the traits studied in the day-neutral lines. The objective of the present study was to determine genetic effects of 16 accessions in five generations (F_5, BC_1F_5, BC_2F_5, BC_3F_5, and BC_4F_5) for agronomic and fiber traits, and to aid cotton breeders in using these accessions in their breeding programs.

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Published in Crop Sci. 38:1428–1431 (1998).

MATERIALS AND METHODS

Day-neutral genes from Deltapine 16 were introgressed into 16 primitive accession with single and multiple backcrosses

Table 1. Predicted main effects of germplasm accessions for yield and fiber traits.

Accession	Lint yield	Lint percentage	Boll size	Seed index	Elongation	Micronaire	50% Span length	2.5% Span length	Strength
	kg ha^{-1}	%	g	g	%		mm	mm	kNm kg^{-1}
T53 (A1)	−21.5	0.23	0.27**	0.01	−0.30**	0.20**	−0.18**	−0.60**	0.07
T78 (A2)	−46.6**	−1.34**	−0.27**	0.05	0.17**	−0.30**	−0.15**	−0.40**	−0.35
T87 (A3)	−9.4	−0.05	0.12*	0.01	0.16**	−0.07	0.04	0.09	3.57*
T88 (A4)	5.4	0.33**	0.32**	0.10*	−0.03	0.05	−0.04	0.31*	−4.25**
T91 (A5)	−76.8**	−1.41**	−0.21**	0.26*	0.07	0.12**	−0.05	−0.36**	5.03**
T106 (A6)	126.2**	0.85**	0.05	−0.09	0.13*	−0.05	0.21**	0.64**	0.41
T119 (A7)	−14.3	−0.25	−0.05	−0.21*	0.03	−0.14**	−0.02	0.12*	−2.25
T158 (A8)	22.4	0.05	0.07**	−0.07	−0.03	0.06	0.03	0.09	−0.42
T168 (A9)	20.1	−0.29*	0.02	−0.11	−0.12**	0.10*	−0.27**	−0.91**	−2.03
T174 (A10)	104.8**	0.78**	−0.05	−0.23*	−0.01	−0.00	0.07	0.43**	1.65
T175 (A11)	20.0	0.41**	0.11	0.15*	0.03	0.08	−0.02	−0.07	−2.30**
T228 (A12)	−53.6**	−1.18**	−0.15**	−0.19*	−0.24**	−0.01	0.01	−0.20**	2.63**
T257 (A13)	−5.8	−0.33	−0.10*	0.10	−0.20**	0.04	0.16**	0.22**	4.18**
T326 (A14)	−30.8*	0.92**	−0.16**	−0.05	0.04	−0.05	0.30**	0.79**	3.47*
T612 (A15)	−41.8**	0.83**	0.12**	0.15*	−0.23**	−0.06*	−0.06	0.11	−6.81**
T1149 (A16)	1.6	0.43**	−0.10*	−0.03	0.53**	0.03	−0.03	−0.25*	−2.63*

***, ** Significantly different from zero at the 0.05 and 0.01 levels of probability, respectively.**

creating 80 populations representing one to four doses of the unadapted accession. The development of the 80 populations were described by McCarty et al. (1995). Experiments were conducted in 1989, 1990, and 1991 in which yield and fiber traits were measured (McCarty et al., 1998).

Data for yield and fiber traits were analyzed by mixed linear model approaches. A linear model was used by including random factors for years as environments (E), accessions (A), generations (G), and their interaction (AG, AE, GE, AGE) along with block factor (B) and residual errors (e). Since random effects can not be estimated, they were predicted by using an adjusted unbiased prediction (AUP) method (Zhu, 1993; Zhu and Weir, 1996). Jackknifing over blocks within years was used to calculate the standard errors of random effects (Miller 1974; Zhu, 1989). Since there were 12 blocks for 3 yr, the degrees of freedom were 11 for the jackknifing. A two-tail t-test was employed for testing significance of genetic parameters studied. All the data analyses were conducted on a PC computer with programs written in C language.

RESULTS AND DISCUSSION

We detected significant accession effects for all the traits studied (Table 1). Accessions 6 (T-106) and 10 (T-174) had large effects for high lint yield, high lint percentage, and long 2.5% span length. Accession 6 also had higher elongation and long 50% span length, while

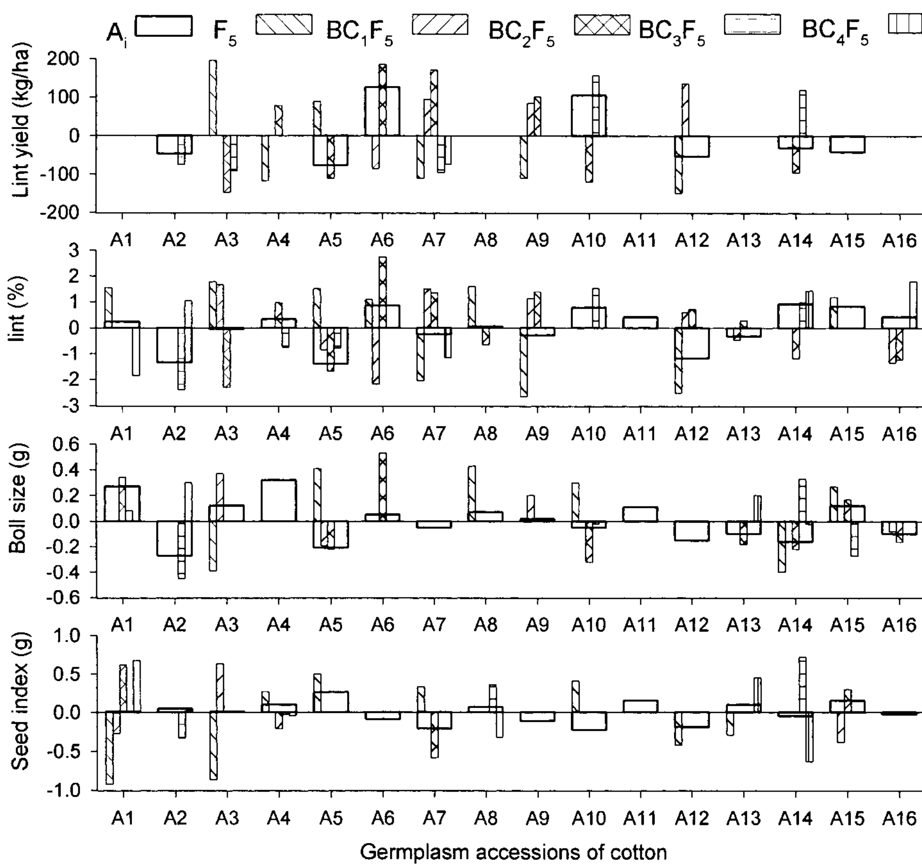

Fig. 1. Predicted interaction effects of accession by generation for yield traits. Wide blank columns is the main effect of accession. Five narrow columns from left to right are generations F_5, BC_1F_5, BC_2F_5, BC_3F_5, and BC_4F_5, respectively.

Table 2. Predicted main effects of generations for yield and fiber traits.†

Generation	Lint yield	Lint percentage	Boll size	Seed index	Elongation	Micronaire	50% Span length	2.5% Span length	Strength
	kg ha^{-1}	%	g		%		mm		kNm kg^{-1}
F_5	73.1**	0.48**	−0.09	−0.09	0.19	−0.11	−0.09	0.00	−2.26
BC_1F_5	56.7*	0.55**	0.12**	0.07	0.06	0.07*	0.01	0.00	−0.78
BC_2F_5	10.1	0.55**	0.02	−0.13	−0.02	−0.01	0.01	0.00	−0.85
BC_3F_5	−71.6*	−0.78**	−0.12**	0.02	−0.18	0.02	−0.00	0.00	1.96
BC_4F_5	−68.2*	−0.79**	0.06*	0.14	−0.05	0.04	0.08	0.00	1.94

*, ** Significantly different from zero at the 0.05 and 0.01 levels of probability, respectively.
† Because of rounding (two decimal places) small contributions of some traits appear as 0.00 in the table.

Accession 10 had small seeds. Accession effects of these two lines were not significant for other yield and fiber traits. Therefore Accessions 6 and 10 may be suitable for utilization in cotton improvement programs. Accession 5 (T-091) had the highest positive main effect for fiber strength but was poor for yield traits and 2.5% span length. Main effects of fiber strength and both span lengths were large for Accession 13 (T-257) which also showed acceptable performance for yield traits. Therefore, Accession 13 may be useful as breeding material for improving both fiber strength and length.

Significant generation main effects were detected for three yield traits but only for one fiber trait (Table 2). The highest lint yield was expected in the F_5 generation which had more genetic background from the high yield cultivar (Deltapine 16) than other generations. Lint yield decreased with more cycles of backcrossing to the accessions. This tendency was not observed for other traits.

Since accession × generation interaction (AG) was the major component of genetic variation for all the traits (McCarty et al., 1998), there could be some deviation for genetic behavior of accessions in different generations. The predicted AG interaction effects along

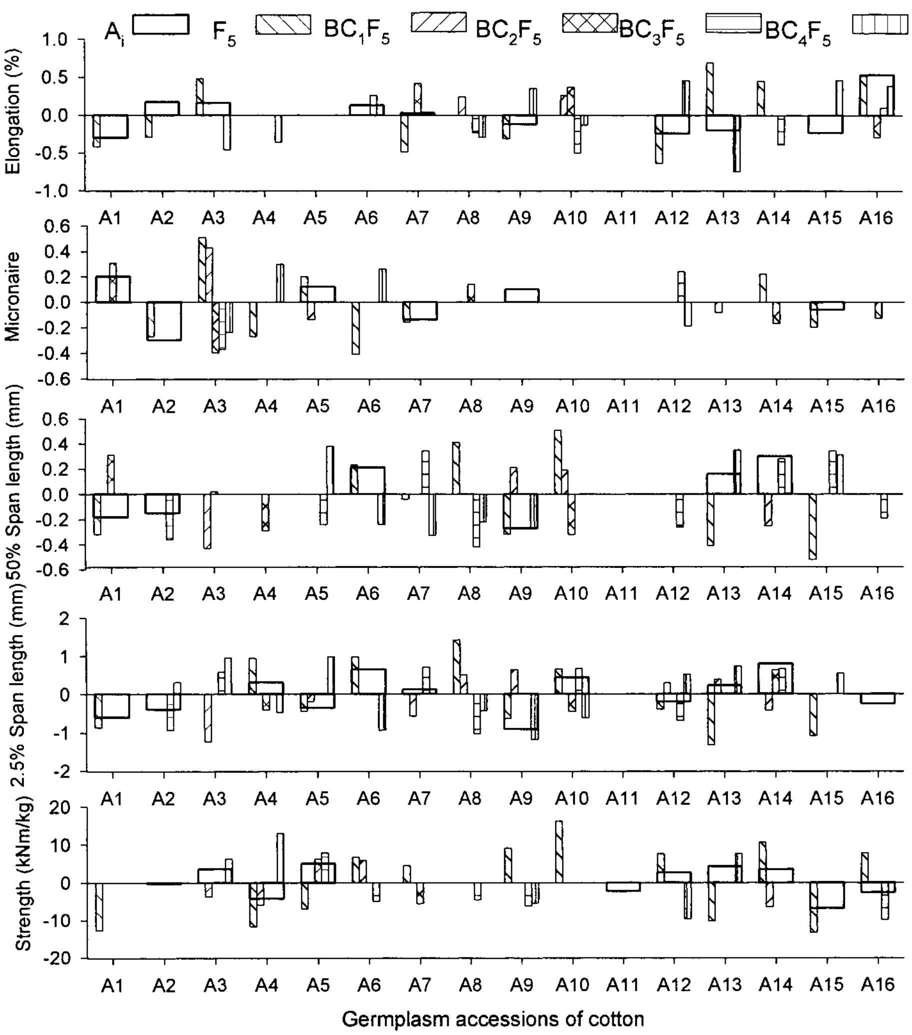

Fig. 2. Predicted interaction effects of accession by generation for fiber traits. Wide blank columns is the main effect of accession. Five small columns from left to right are generations F_5, BC_1F_5, BC_2F_5, BC_3F_5, and BC_4F_5, respectively.

with the accession main effects, which were significantly different from zero ($P \leq 0.05$), are presented in Fig. 1 for yield traits and in Fig. 2 for fiber traits. Although main accession effects of lint yield were large for Accessions 6 and 10, not all the generations in these two accessions were equally important for improving yield. BC_1F_5 in Accession 6 and BC_2F_5 in Accession 10 tended to decrease yield by about 100 kg ha^{-1}, while BC_2F_5 in Accession 6 and BC_3F_5 in Accession 10 increased yield over 150 kg ha^{-1}. The yield gain of BC_2F_5 in Accession 6 was due to the high lint percentage and large bolls, while high yield of BC_3F_5 in Accession 10 might be the result of high lint percentage and median size of boll (indicating large number of bolls). Although Accession 3 (T-087) had positive main effects for boll size but not for lint yield and lint percentage, F_5 in Accession 3 had high lint yield with very small boll (indicating large number of bolls) and high lint percentage. It was implied by this analysis that F_5 in Accession 3 was a different type of high yield material as compared with BC_2F_5 in Accession 6. Genetic entries derived from these two materials might be further used as two parents of a cross which might result in higher yield.

Though Accession 13 tended to have strong and long fiber because of the positive main effects, it was not true for its F_5 generation. Actually BC_4F_5 in Accession 13 was good for fiber strength and both span lengths. It was found by the AG interaction analysis that F_5 in Accession 10 had stronger and longer fiber also with large value of boll size and seed index. Therefore, F_5 in Accession 10 and BC_2F_5 in Accession 6 could serve as a breeding material for further improving fiber quality of cotton.

When there are significant accession main effects and accession $\times$ generation interaction effects, the genetic merit of an accession in a specific generation is determined by the sum of main and interaction effects (A + AG). In the present study, Accession 6, in BC_2F_5 proved to make the highest contribution to yield with a 312 kg ha^{-1} increase over the population mean. The yield components lint percentage and boll size contributed to the improved yield of BC_2F_5 of Accession 6. The genetic entry with the strongest fiber was found from F_5 of Accession 10, which increase fiber strength by about 17.9 kNm kg^{-1}. Accession 10 also increased 2.5% span length (1.09 mm), 50% span length (0.58 mm), and even lint yield (108 kg ha^{-1}) in the F_5 generation.

Genotype, environment, and their interaction affected the phenotypic behavior of genetic entries derived from primitive accessions of cotton. It was revealed that genetic analysis of the primitive accession of cotton could result in a better understanding of the breeding merit for specific mating generations of different accessions.

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